GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:07:02 ; Search time 755.06 Seconds
(without alignments)
28.386 Million cell updates/sec

Title: US-09-851-670-17
Perfect score: 25
Sequence: 1 ctccaacttggaatcacggtacaca 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	14.6	58.4	25	22	AAC86088	5' Primer RC978 to
c	2	14.6	58.4	28	18	AAT66338	3' primer for DNA
	3	14.6	58.4	59	18	AAV76019	Staphylococcus aur
	4	14.4	57.6	39	16	AAQ81380	Forward primer for
	5	14.4	57.6	39	18	AAT49185	Murine IgG heavy c
	6	14.4	57.6	39	21	AAC84070	Murine Ig heavy ch
	7	14.4	57.6	60	20	AAZ22294	Probe Seq ID No: 4
	8	14.4	57.6	60	20	AAV84047	Primer used in met
c	9	14.2	56.8	42	18	AAT92137	Clone pPD74.29 fro
	10	14	56.0	50	14	AAQ43347	Sequence of PCR pr
c	11	13.8	55.2	47	21	AAZ66275	Human map-related
c	12	13.8	55.2	47	21	AAZ66603	Human map-related
c	13	13.8	55.2	56	14	AAQ43346	Sequence of PCR pr
	14	13.8	55.2	58	18	AAT57993	Truncated P-select
	15	13.6	54.4	21	21	AAA96649	PCR primer for a c
c	16	13.4	53.6	40	14	AAQ43345	Sequence of PCR pr
	17	13.4	53.6	50	14	AAQ43353	Sequence of PCR pr
c	18	13.4	53.6	51	14	AAQ43354	Sequence of PCR pr
c	19	13.4	53.6	52	14	AAQ43351	Sequence of PCR pr
c	20	13.4	53.6	53	14	AAQ43349	Sequence of PCR pr
	21	13.4	53.6	56	14	AAQ43344	Sequence of PCR pr
c	22	13.4	53.6	57	14	AAQ43342	Sequence of PCR pr
	23	13.2	52.8	24	18	AAV01258	T-cell receptor al
	24	13.2	52.8	30	13	AAQ25323	5' PCR primer for
	25	13.2	52.8	36	21	AAA10714	PCR primer B5RL us
c	26	13	52.0	21	21	AAA52944	Mouse EphA4 gene P
	27	13	52.0	30	17	AAV06695	Oligonucleotide RB
	28	13	52.0	30	17	AAT31364	Human immunodefici
	29	13	52.0	30	19	AAV07588	Nucleotide sequenc
	30	13	52.0	30	19	AAV07591	Nucleotide sequenc
	31	13	52.0	31	19	AAV26300	Human prostate can
	32	13	52.0	31	20	AAX26039	Prostate disease m
c	33	13	52.0	47	19	AAV07585	Nucelotide sequenc
c	34	12.8	51.2	20	21	AAA93946	PCR primer used to
c	35	12.8	51.2	21	21	AAA39745	Potato cv. Cara in
	36	12.8	51.2	29	21	AAA63760	PCR primer used to
	37	12.8	51.2	30	13	AAQ29831	Multi locus detect
	38	12.8	51.2	30	18	AAT70567	Group specific com
c	39	12.8	51.2	31	21	AAA72200	Human aldolase A P
c	40	12.8	51.2	32	21	AAZ55318	Neisseria species
c	41	12.8	51.2	39	21	AAA12112	T. brucei trypanos
c	42	12.8	51.2	57	22	AAF75833	Porcine circovirus
c	43	12.8	51.2	57	22	AAF28305	PCV1 ORF1 PCR prim
c	44	12.6	50.4	20	18	AAV03702	Primer SHF-15 for
c	45	12.6	50.4	20	21	AAA78224	Anti-human Fas ant

ALIGNMENTS

RESULT 1
AAC86088/c
ID AAC86088 standard; DNA; 25 BP.
XX
AC AAC86088;
XX
DT 29-AUG-2001 (first entry)
XX
DE 5' Primer RC978 to amplify LZ-1 in transgenic plants.
XX
KW Transcription factor stress-related protein; TFSRP; stress-tolerance;
KW CAAT-box like binding factor; CABF; DNA binding factor; DBF; primer;
KW homeo domain/leucine zipper; HDZ; zinc-finger; ZF; leucine zipper; LZ;
KW CABF-1; CABF-2; DBF-1; CRT/DRE binding factor-1; CBF-1; HDZ-1; ZF-1;
KW LZ-1; transgenic plant; environmental stress; drought; salinity; PCR;
KW temperature; metal; chemical; pathogen; oxidative stress; amplify;
KW polymerase chain reaction; expressed sequence tag; EST; RACE PCR;
KW Physcomitrella patens; RT-PCR; ss.
XX
OS Synthetic.
XX
PN WO200145493-A2.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US34972.
XX
PR 22-DEC-1999; 99US-0171745.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Costa e Silva OD, Van Thielen N, Chen R;
XX
DR WPI; 2001-417953/44.

```
XX
PT   Novel transcription factor stress-related protein and nucleic acid
PT   encoding the proteins, for producing transgenic plants having increased
PT   tolerance to environmental stress including salinity, drought and
PT   temperature -
XX
PS   Example 9; Page 71; 115pp; English.
XX
CC   The sequences given in AAC86082-101 are primers which were used to
CC   amplify DNA's encoding transcription factor stress-related proteins
CC   (TFSRP's) from Physcomitrella patens, as transgenes in transgenic
CC   plants.  TFSRP's are used for conferring stress-tolerance in plants.
CC   The TFSRP's of the invention are selected from CAAT-box like binding
CC   factor (CABF), DNA binding factor (DBF), homeo domain/leucine zipper
CC   (HDZ), zinc-finger (ZF) and leucine zipper (LZ), preferably CABF-1,
CC   CABF-2, DBF-1, CRT/DRE binding factor-1 (CBF-1), HDZ-1, ZF-1, LZ-1,
CC   or their homologs.  The nucleic  acid encoding the TFSRP's are useful
CC   for producing transgenic plants, with increased tolerance to
CC   environmental stress, including drought, salinity or temperature,
CC   as compared to a wild type variety of the plant.  TFSRP nucleic
CC   acid is also useful for increasing the expression of a gene of
CC   interest within a host cell as compared to a wild-type variety of a host
CC   cell, by transforming the host cell with an expression vector comprising
CC   the TFSRP coding nucleic acid and expressing TFSRP in the cell.
CC   The environmental stress can also be metal, chemical, pathogenic and
CC   oxidative stresses or their combinations. TFSRP nucleic acid molecules,
CC   proteins, vectors and host cells are useful for identification and
CC   mapping of genomes of P.patens and related organisms, identification
CC   and localization of P.patens sequences of interest, evolutionary and
CC   protein structural studies, determination of TFSRP regions required for
CC   function, modulation of a TFSRP activity, metabolism of one or more
CC   cell functions, transmembrane transport of one or more compounds and
CC   stress resistance. TFSRP protein and nucleic acid molecules also serve
CC   as markers for specific regions of the genome and to generate algae,
CC   ciliates, plants, fungi or other microorganisms expressing mutated
CC   TFSRP nucleic acid and protein molecules such that the stress tolerance
CC   is improved.
XX
SQ   Sequence 25 BP; 6 A; 3 C; 11 G; 5 T; 0 other;


  Query Match             58.4%;  Score 14.6;  DB 22;  Length 25;
  Best Local Similarity   81.0%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 ccaacttggaatcacggtaca 23
           ||||||| | ||||| || ||
Db      25 CCAACTTCGCATCACCGTCCA 5


RESULT   2
AAT66338/c
ID   AAT66338 standard; DNA; 28 BP.
XX
AC   AAT66338;
XX
DT   11-NOV-1997  (first entry)
XX
DE   3' primer for DNA of upstream region of tobacco 16S rDNA.
XX
KW   Upstream region; tobacco; 16S rDNA; plastid; DNA construct;
KW   stable transformation; multicellular plant; transcription;
KW   nucleus encoded; RNA polymerase; tissue specific; expression;
KW   polymerase chain reaction; primer; amplification; PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9706250-A1.
XX
PD   20-FEB-1997.
XX
PF   01-AUG-1996;   96WO-US12671.
XX
PR   10-AUG-1995;   95US-0002136.
XX
PA   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
PI   Allison LA,  Hajdukiewicz PT,  Maliga P;
XX
DR   WPI; 1997-154257/14.
XX
PT   Construct contg. promoter recognised by nucleus-encoded plastid RNA
PT   polymerase - provides tissue specific expression of heterologous
PT   genes for stable transformation of plastid(s) in higher plants
XX
PS   Example 1; Page 16; 55pp; English.
XX
CC   The present sequence, a primer for the PCR amplification of the
CC   DNA of the upstream region of a tobacco 16S rDNA (nucleotides -201
CC   to -1), is complementary to nucleotides 102761 to 102742 of the
CC   tobacco plastid genome. The upstream region was used in the
CC   development of a novel DNA construct for the stable transformation
CC   of plastids in multicellular plants, which comprises a transforming
CC   DNA having a target sequence for insertion into the plastid genome
CC   by homologous recombination, a selectable marker gene providing a
CC   selectable phenotype to cells containing transformed plastids, a
CC   cloning site for inserting a gene of interest and a 5'-promoter
CC   element that is recognised and transcribed by a nucleus encoded
CC   plastid RNA polymerase. The construct provides plant tissue, e.g.
CC   root, seed or meristem tissue, specific expression of a gene of
CC   interest, e.g. a gene that makes roots toxic or repellent to
CC   nematodes or controls oil production in seeds. The construct can
CC   be used to transform a wider range of plant species than known
CC   systems.
XX
SQ   Sequence 28 BP; 7 A; 7 C; 6 G; 8 T; 0 other;


  Query Match             58.4%;  Score 14.6;  DB 18;  Length 28;
  Best Local Similarity   81.0%;  Pred. No. 5.1e+02;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 tccaacttggaatcacggtac 22
           | |||||  ||||| ||||||
Db      24 TGCAACTATGAATCTCGGTAC 4


RESULT   3
AAV76019
ID   AAV76019 standard; DNA; 59 BP.
XX
AC   AAV76019;
XX
DT   16-MAR-1999  (first entry)
XX
DE   Staphylococcus aureus contig SEQ ID #1708.
XX
KW   Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW   cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
KW   skin infection; surgical wound infection; scalded skin syndrome;
KW   toxic shock syndrome; ds.
XX
OS   Staphylococcus aureus.
XX
PN   EP786519-A2.
XX
PD   30-JUL-1997.
XX
PF   07-JAN-1997;   97EP-0100117.
XX
PR   05-JAN-1996;   96US-0009861.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Barash SC,  Choi GH,  Dillon PJ,  Fannon MR,  Kunsch CA;
PI   Rosen CA;
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XX
DR WPI; 1997-374922/35.
XX
PT Polynucleotide(s) and proteins derived from Staphylococcus aureus -
PT stored on computer readable medium and used in the production of
PT anti-S.aureus vaccines
XX
PS Claim 1; Page 2038; 3271pp; English.
XX
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.
XX
SQ Sequence 59 BP; 20 A; 6 C; 6 G; 27 T; 0 other;

Query Match 58.4%; Score 14.6; DB 18; Length 59;
Best Local Similarity 81.0%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 aacttggaatcacggtacaca 25
|| || |||| || |||||||
Db 1 aaatttgaataactgtacaca 21

RESULT 4
AAQ81380
ID AAQ81380 standard; DNA; 39 BP.
XX
AC AAQ81380;
XX
DT 21-AUG-1995 (first entry)
XX
DE Forward primer for the IgG signal sequence.
XX
KW PCR primer; IgG signal sequence; ss.
XX
OS Synthetic.
XX
PN WO9503408-A.
XX
PD 02-FEB-1995.
XX
PF 26-JUL-1994; 94WO-US08423.
XX
PR 26-JUL-1993; 93US-0101624.
PR 19-AUG-1993; 93US-0109393.
PR 03-NOV-1993; 93US-0147773.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (REPK) REPLIGEN CORP.
XX
PI Freeman GJ, Gray GS, Greenfield E, Nadler LM;
XX
DR WPI; 1995-075236/10.
XX
PT Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
PT for enhancing or suppressing T-cell mediated immune responses
XX
PS Example; Page 84; 175pp; English.
XX
CC PCR amplification was used to generate an immunoglobulin signal
CC sequence suitable for secretion of the B7-2Ig fusion protein
CC from mammalian cells. The Ig signal sequence was prepd. from
CC a plasmid contg. the murine IgG heavy chain gene using AAQ81380 as
CC the foward primer and AAQ81381 as the reverse PCR primer. The forward
CC PCR primer contain recognition site for BsaI and is homologous to
CC sequences 5' to the initiating Met of the Ig signal sequence. The
CC reverse primer is composed of sequences derived from the 5' end of
CC the extracellular domain of hB7-2 and the 3' end of the Ig
CC signal sequence.
XX
SQ Sequence 39 BP; 8 A; 12 C; 8 G; 11 T; 0 other;

Query Match 57.6%; Score 14.4; DB 16; Length 39;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ctccaacttggaatcacggtacac 24
||||| |||| ||||| || | |
Db 11 ctccagcttgagatcacagttctc 34

RESULT 5
AAT49185
ID AAT49185 standard; DNA; 39 BP.
XX
AC AAT49185;
XX
DT 08-APR-1997 (first entry)
XX
DE Murine IgG heavy chain signal sequence PCR primer 1.
XX
KW CTLA4; CD28; ligand; B7-2; B lymphocyte antigen; B-cell;
KW costimulation; immunoglobulin; antibody; autoimmune disease;
KW allergy; tumour; vaccine; graft versus host disease; T-cell;
KW T lymphocyte; TH2 response; immunosuppressive; immunostimulant;
KW therapy; IgG; polymerase chain reaction; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9640915-A2.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09052.
XX
PR 07-JUN-1995; 95US-0479744.
XX
PA (DAND) DANA FARBER CANCER INST INC.
PA (REPK) REPLIGEN CORP.
XX
PI Freeman GJ, Gray GS, Nadler LM;
XX
DR WPI; 1997-077269/07.
XX
PT DNA encoding a B7-2 fusion protein - used to enhance or down
PT regulate B lymphocyte antigens
XX
PS Example 7; Page 72; 171pp; English.
XX
CC PCR amplification was used to generate an IgG signal sequence
CC suitable for secretion of B7-2Ig fusion protein from mammalian
CC cells. Forward primer 1 (AAT49185) contains recognition sequences
CC for BsaI and is homologous to sequences 5' to the initiating
CC methionine of the murine IgG heavy chain signal sequence. Reverse
CC primer 2 (AAT49186) is composed of sequences derived from the 5' end
CC of the extracellular domain of human B-cell antigen B7-2 (see also
CC AAT49181) and the 3' end of the Ig signal sequence. The PCR product
CC (224 bp) is composed of BsaI sites followed by the Ig signal

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CC   sequence fused to the first 20 nucleotides of the coding sequence
CC   of the B7-2 extracellular domain.  B7-2Ig fusion proteins can be
CC   used to enhance or down-regulate B lymphocyte antigens.
XX
SQ   Sequence 39 BP; 8 A; 12 C; 8 G; 11 T; 0 other;


  Query Match             57.6%;  Score 14.4;  DB 18;  Length 39;
  Best Local Similarity   75.0%;  Pred. No. 6.7e+02;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 ctccaacttggaatcacggtacac 24
           ||||| ||||  ||||| || | |
Db      11 ctccagcttgagatcacagttctc 34


RESULT   6
AAC84070
ID   AAC84070 standard; DNA; 39 BP.
XX
AC   AAC84070;
XX
DT   28-MAR-2001  (first entry)
XX
DE   Murine Ig heavy chain gene signal sequence forward primer.
XX
KW   Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
KW   antigen; extracellular domain; CTLA4; immunoglobulin constant region;
KW   immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
KW   T cell-mediated immune response; transplantation; vaccination;
KW   PCR primer; fusion construct; ss.
XX
OS   Mus sp.
XX
PN   US6130316-A.
XX
PD   10-OCT-2000.
XX
PF   26-JUL-1994;   94US-0280757.
XX
PR   26-JUL-1993;   93US-0101624.
PR   19-AUG-1993;   93US-0109393.
PR   03-NOV-1993;   93US-0147773.
XX
PA   (DAND ) DANA FARBER CANCER INST INC.
PA   (REPK ) REPLIGEN CORP.
XX
PI   Freeman GJ,  Nadler LM,  Gray GS,  Greenfield E;
XX
DR   WPI; 2000-655681/63.
XX
PT   Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
PT   enhancing or suppressing T cell-mediated immune responses, especially
PT   during tissue, skin or organ transplantation, or in graft-versus-host
PT   disease -
XX
PS   Example 7; Column 55; 83pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule encoding a
CC   fusion protein comprising a first nucleotide sequence encoding a first
CC   peptide, and a second nucleotide sequence encoding a second peptide.
CC   The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
CC   citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
CC   to a portion of a nucleotide sequence which encodes a human or murine
CC   B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
CC   the ability to bind CD28 or CTLA4. The first peptide has an amino acid
CC   sequence that is identical or at least 50% identical with the
CC   extracellular domain of a human B7-2 peptide (AAB37085). The second
CC   peptide is especially an immunoglobulin constant region. Primers
CC   AAC84070-C84071 were used to PCR amplify the signal peptide sequence from
CC   the murine IgG gene. The signal peptide sequence was used to generate an
CC   hB7-2/Ig fusion construct. The nucleic acid molecules are useful in
CC   various expression vectors to direct synthesis of the corresponding
CC   proteins or peptides in a variety of hosts, particularly eukaryotic
CC   cells, e.g. mammalian or insect cell culture. The nucleic acids are also
CC   useful for enhancing the immunogenicity of a mammalian cell, e.g. tumour
CC   cell (sarcoma) or an antigen presenting cell (macrophage). The fusion
CC   proteins or peptides are useful for enhancing or suppressing T
CC   cell-mediated immune responses, e.g. in situations of tissue, skin or
CC   organ transplantation, or in graft-versus-host disease. The proteins are
CC   also useful for enhancing the efficacy of vaccination against a variety
CC   of pathogens, and may also be used to upregulate an immune response
CC   against a particular pathogen during an infection or against a tumour in
CC   a tumour-bearing host.
XX
SQ   Sequence 39 BP; 8 A; 12 C; 8 G; 11 T; 0 other;


  Query Match             57.6%;  Score 14.4;  DB 21;  Length 39;
  Best Local Similarity   75.0%;  Pred. No. 6.7e+02;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 ctccaacttggaatcacggtacac 24
           ||||| ||||  ||||| || | |
Db      11 ctccagcttgagatcacagttctc 34


RESULT   7
AAZ22294
ID   AAZ22294 standard; DNA; 60 BP.
XX
AC   AAZ22294;
XX
DT   20-DEC-1999  (first entry)
XX
DE   Probe Seq ID No: 4 of WO9950401.
XX
KW   Intracellular gene expression; fluorescent; labeling; hybridization;
KW   screening; multi-probe DNA binding genome chip; probe; ss.
XX
OS   Synthetic.
XX
PN   WO9950401-A1.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-JP01574.
XX
PR   27-MAR-1998;   98JP-0100096.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Muramatsu M,  Wakao H,  Wakao R,  Yano K,  Noguchi T,  Suyama A;
XX
DR   WPI; 1999-580760/49.
XX
PT   Detection of gene expression with fluorescent labels, useful for
PT   screening genes and compounds capable of changing specific gene
PT   expression -
XX
PS   Disclosure; Page 12; 26pp; Japanese.
XX
CC   The invention relates to a method for detecting a change in
CC   intracellular gene expression induced by treatment with a specific
CC   compound. The method comprises (a) isolating intracellular mRNAs from
CC   treated and untreated cells; (b) transcribing the isolated mRNAs to give
CC   cDNA groups; (c) applying different fluorescent labeling to the cDNA
CC   groups; (d) hybridizing the respective labeled cDNA groups with specific
CC   probe DNAs; and (e) measuring the difference in contents of cDNAs based
CC   on the generated fluorescence after hybridization. The method is useful
CC   for screening for a gene whose expression is changed by treatment with a
CC   specific compound, or screening for a compound capable of changing the
CC   expression of a specific gene. The method is convenient and efficient
CC   because labeling with different fluorescent substances can be
CC   incorporated to aid detection of changes, including the application of a
CC   multi-probe DNA binding genome chip. Sequences AAZ22291-96 represent
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CC   oligonucleotide probes used during the course of the invention.
XX
SQ   Sequence 60 BP; 13 A; 19 C; 15 G; 13 T; 0 other;


  Query Match             57.6%;  Score 14.4;  DB 20;  Length 60;
  Best Local Similarity   75.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 ctccaacttggaatcacggtacac 24
          ||||| | |||  |||| || |||
Db      4 ctccatcctggcctcactgtccac 27


RESULT   8
AAV84047
ID   AAV84047 standard; DNA; 60 BP.
XX
AC   AAV84047;
XX
DT   05-MAR-1999  (first entry)
XX
DE   Primer used in method for detecting changes in gene expression.
XX
KW   Gene expression; gene screening; foreign gene; gene selection;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   WO9849282-A1.
XX
PD   05-NOV-1998.
XX
PF   27-APR-1998;   98WO-JP01935.
XX
PR   28-APR-1997;   97JP-0111635.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Muramatsu M,  Noguchi T,  Suyama A,  Yano K;
XX
DR   WPI; 1999-024052/02.
XX
PT   Effective detection of changes in gene expression in cells caused by
PT   transfer of gene, including synthetic, to be tested by extracting
PT   mRNAs then comparing with those from control in constitution - for
PT   screening gene expression affected by introduced foreign gene
PT   expression, suitable e.g. in genome chip method, to isolate genes
PT   with unknown functions for further studies
XX
PS   Example 1; Page 11; 23pp; English.
XX
CC   The present primer is used in the method of the invention. The method
CC   is for detecting changes in gene expression in cells caused by the
CC   expression of a gene to be tested. The method comprises extracting
CC   mRNAs from cells into which the gene to be tested has been transferred,
CC   and from control cells with no test gene inserted, followed by comparing
CC   theses mRNAs in constitution. The method can be used to detect changes
CC   in gene expression in cells caused by introduced gene, for screen genes
CC   suffering from changes in their expression due to the presence of a
CC   foreign gene, in gene selection for study of its function.
XX
SQ   Sequence 60 BP; 13 A; 19 C; 15 G; 13 T; 0 other;


  Query Match             57.6%;  Score 14.4;  DB 20;  Length 60;
  Best Local Similarity   75.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 ctccaacttggaatcacggtacac 24
          ||||| | |||  |||| || |||
Db      4 ctccatcctggcctcactgtccac 27


RESULT   9
AAT92137/c
ID   AAT92137 standard; DNA; 42 BP.
XX
AC   AAT92137;
XX
DT   02-FEB-1998  (first entry)
XX
DE   Clone pPD74.29 from rolling circle replication on template zf42.
XX
KW   Oligonucleotide; concatamer; library; annealing; ligation; single strand;
KW   circular template; primer; rolling circle replication; double strand;
KW   cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   repeat_unit     12..27
FT                   /*tag=  a
XX
PN   US5648245-A.
XX
PD   15-JUL-1997.
XX
PF   09-MAY-1995;   95US-0437538.
XX
PR   09-MAY-1995;   95US-0437538.
XX
PA   (CARN-) CARNEGIE INST WASHINGTON.
XX
PI   Fire A,  Xu S;
XX
DR   WPI; 1997-372060/34.
XX
PT   Construction of oligo:nucleotide concatamer library - by rolling
PT   circle replication of primer bridged circular template
XX
PS   Disclosure; Fig 5B; 21pp; English.
XX
CC   This sequence represents the monomeric repeat unit in clone pPD74.29,
CC   resulting from rolling circle replication on the template zf42
CC   (AAT92127). The template is formed by annealing the 5' and 3' regions of
CC   the template oligonucleotide to a separate oligonucleotide such that the
CC   5' terminal nucleotide is annealed adjacent to the 3' nucleotide of the
CC   same molecule and these can be ligated to generate a single stranded
CC   circular template upon which an oligonucleotide primer is hybridised.
CC   The annealed primer can then act as an initiation primer for a rolling
CC   circle mechanism of replication.  This leads to the formation of a long
CC   single stranded concatamer of the template, including sequences of
CC   interest inserted between the ends of the template oligonucleotide.  The
CC   single stranded concatamers are subsequently converted to double strands
CC   and the sequences of interest are cloned.
XX
SQ   Sequence 42 BP; 11 A; 10 C; 9 G; 12 T; 0 other;


  Query Match             56.8%;  Score 14.2;  DB 18;  Length 42;
  Best Local Similarity   84.2%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 ctccaacttggaatcacgg 19
          ||| |||||||||  ||||
Db     24 CTCAAACTTGGAACTACGG 6


RESULT  10
AAQ43347
ID   AAQ43347 standard; DNA; 50 BP.
XX
AC   AAQ43347;
XX
DT   13-SEP-1993  (first entry)
```

```
XX
DE   Sequence of PCR primer EBI-3776 for the construction of
DE   plasmid pAdneo(3xTREd16)BGluci.
XX
KW   PCR; primer; oligonucleotide.
XX
OS   Synthetic.
XX
PN   WO9311257-A.
XX
PD   10-JUN-1993.
XX
PF   25-NOV-1992;   92WO-EP02718.
XX
PR   25-NOV-1991;   91DE-4138621.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI   Czernilofsky AP,  Himmler A,  Stratowa C,  Weyer U;
PI   Lamche H,  Schaefer R;
XX
DR   WPI; 1993-197073/24.
XX
PT   Screening substances that modulate receptor-dependent signal
PT   transmission path - using test cells transformed with reporter
PT   gene and regulatory sequence sensitive to
PT   inositol-1,4,5-tri:peptide and di:acyl:glycerine(s)
XX
PS   Example; Page 53; 170 pp; German.
XX
CC   pAdneo contains the Neomycin-phosphotransferase gene under the
CC   control of SV40 early promoters and SV40 polyA signals. The
CC   promoter region of the thymidine kinase gene of herpes simplex
CC   virus type I flanked by two polycloning sites was introduced into
CC   plasmid pADneo. PADneoBGluci was constructed using oligos EBI-3182
CC   and EBI-3184 to introduce the beta-globin promoter. pADneo(3TRE)
CC   BGluci contains three TPA responsive elements (TREs) constructed
CC   using nucleotide pairs EBI-3677/3671 and EBI-3672/3678. Plasmid
CC   pADneo(3xTREd16) contains 3 TRE elements separated from each other
CC   by 16 bases. It is constructed using EBI-3775 and complementary
CC   oligo EBI-3671, EBI-3776 and complementary oligo EBI-3777.
XX
SQ   Sequence 50 BP; 15 A; 14 C; 8 G; 13 T; 0 other;


  Query Match             56.0%;  Score 14;  DB 14;  Length 50;
  Best Local Similarity   77.3%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       4 caacttggaatcacggtacaca 25
           | || | ||||||||||  |||
Db       2 cgaccttgaatcacggtctaca 23


RESULT  11
AAZ66275/c
ID   AAZ66275 standard; DNA; 47 BP.
XX
AC   AAZ66275;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:622.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 1; Page 363; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 13 A; 13 C; 10 G; 11 T; 0 other;


  Query Match             55.2%;  Score 13.8;  DB 21;  Length 47;
  Best Local Similarity   72.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ctccaacttggaatcacggtacaca 25
             ||   ||  || |||||||||| |||
Db      35 CTTGTACCAGGTATCACGGTAAACA 11


RESULT  12
AAZ66603/c
ID   AAZ66603 standard; DNA; 47 BP.
XX
AC   AAZ66603;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:950.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,G)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
```

```
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 1; Page 433; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 7 A; 9 C; 14 G; 17 T; 0 other;


  Query Match             55.2%;  Score 13.8;  DB 21;  Length 47;
  Best Local Similarity   72.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ctccaacttggaatcacggtacaca 25
           | |||||  ||||||  | || |||
Db      37 CGCCAACAAGGAATCCTGATAGACA 13


RESULT  13
AAQ43346/c
ID   AAQ43346 standard; DNA; 56 BP.
XX
AC   AAQ43346;
XX
DT   13-SEP-1993  (first entry)
XX
DE   Sequence of PCR primer EBI-3775 for the construction of
DE   plasmid pAdneo(3xTREd16)BGluci.
XX
KW   PCR; primer; oligonucleotide.
XX
OS   Synthetic.
XX
PN   WO9311257-A.
XX
PD   10-JUN-1993.
XX
PF   25-NOV-1992;   92WO-EP02718.
XX
PR   25-NOV-1991;   91DE-4138621.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI   Czernilofsky AP,  Himmler A,  Stratowa C,  Weyer U;
PI   Lamche H,  Schaefer R;
XX
DR   WPI; 1993-197073/24.
XX
PT   Screening substances that modulate receptor-dependent signal
PT   transmission path - using test cells transformed with reporter
PT   gene and regulatory sequence sensitive to
PT   inositol-1,4,5-tri:peptide and di:acyl:glycerine(s)
XX
PS   Example; Page 52; 170 pp; German.
XX
CC   pAdneo contains the Neomycin-phosphotransferase gene under the
CC   control of SV40 early promoters and SV40 polyA signals. The
CC   promoter region of the thymidine kinase gene of herpes simplex
CC   virus type I flanked by two polycloning sites was introduced into
CC   plasmid pADneo. PADneoBGluci was constructed using oligos EBI-3182
CC   and EBI-3184 to introduce the beta-globin promoter. pADneo(3TRE)
CC   BGluci contains three TPA responsive elements (TREs) constructed
CC   using nucleotide pairs EBI-3677/3671 and EBI-3672/3678. Plasmid
CC   pADneo(3xTREd16) contains 3 TRE elements separated from each other
CC   by 16 bases. It is constructed using EBI-3775 and complementary
CC   oligo EBI-3671, EBI-3776 and complementary oligo EBI-3777.
XX
SQ   Sequence 56 BP; 14 A; 13 C; 16 G; 13 T; 0 other;


  Query Match             55.2%;  Score 13.8;  DB 14;  Length 56;
  Best Local Similarity   72.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 ctccaacttggaatcacggtacaca 25
           | | ||  | ||||||||||  |||
Db      51 CACTAAGCTTGAATCACGGTCTACA 27


RESULT  14
AAT57993
ID   AAT57993 standard; RNA; 58 BP.
XX
AC   AAT57993;
XX
DT   01-DEC-1997  (first entry)
XX
DE   Truncated P-selectin family 5 SELEX ligand PF411.
XX
KW   Identification; ligand; lectin; SELEX; wheat germ agglutinin; template;
KW   Systematic Evolution of Ligands by EXponential enrichment; amplification;
KW   primer; PCR; polymerase chain reaction; peritoneal inflammation; ss;
KW   diabetes; lymphocyte trafficking disorder; glomerulonephritis; arthritis.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1..58
FT                    /*tag=  a
FT                    /mod_base= all C bases are 2' Fluoro-cytosine
FT                    /mod_base= all U bases are 2' Fluoro-uracil
XX
PN   WO9640703-A1.
XX
PD   19-DEC-1996.
XX
PF   05-JUN-1996;   96WO-US09455.
XX
PR   07-JUN-1995;   95US-0479724.
PR   07-JUN-1995;   95US-0472255.
PR   07-JUN-1995;   95US-0472256.
PR   07-JUN-1995;   95US-0477829.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
```

XX
PI Bridonneau P, Gold L, Hicke B, Parma DH;
XX
DR WPI; 1997-077252/07.
XX
PT Identifying nucleic acid ligands that bind lectin(s) esp.
PT selectin(s) - by partitioning the ligands from a mixture of nucleic
PT acids
XX
PS Claim 48; Page 186; 255pp; English.
XX
CC The invention relates to the identification of nucleic acid ligands to
CC a lectin using the Systematic Evolution of Ligands by EXponential
CC enrichment (SELEX) method. The sequences AAT57963-T58039 represent RNA
CC ligands isolated by the method which bind to P-selectin. The P-selectin
CC ligands were isolated from a DNA template containing 50 random
CC nucleotides flanked by fixed 5' and 3' sequences (AAT58049), which was
CC amplified using the primers AAT58050-1. The ligands fall into 5 major
CC families along with 2 groups of unrelated 'orphan' ligands. No binding
CC affinity of this ligand for P-selectin is given in the specification.
CC The ligands are especially useful in the treatment of peritoneal
CC inflammation, diabetes, lymphocyte trafficking disorders,
CC glomerulonephritis, arthritis, etc.
XX
SQ Sequence 58 BP; 20 A; 15 C; 13 G; 10 U; 0 other;

Query Match 55.2%; Score 13.8; DB 18; Length 58;
Best Local Similarity 56.0%; Pred. No. 1.4e+03;
Matches 14; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ctccaacttggaatcacggtacaca 25
|: | |:: ||| || ||:| |||
Db 6 cuagagcuucgaaccaugguauaca 30

RESULT 15
AAA96649
ID AAA96649 standard; DNA; 21 BP.
XX
AC AAA96649;
XX
DT 08-FEB-2001 (first entry)
XX
DE PCR primer for a cDNA fragment encoding a human Akt3 polypeptide.
XX
KW Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;
KW hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;
KW reperfusion injury; myocardial ischemia reperfusion injury; stroke;
KW liver damage; renal failure; organ transplantation; coronary artery;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200056866-A2.
XX
PD 28-SEP-2000.
XX
PF 14-MAR-2000; 2000WO-US06574.
XX
PR 19-MAR-1999; 99US-0125108.
XX
PA (AVET) AVENTIS PHARM PROD INC.
XX
PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
XX
DR WPI; 2000-638260/61.
XX
PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic
PT cell death induced by apoptosis stimulating kinase 1 useful for
PT treating myocardial infarction or ischemia reperfusion injury -
XX
PS Example 1; Page 41; 73pp; English.
XX
CC PCR primers AAA96648-49 were used to amplify cDNA encoding a human Akt3
CC protein. Expression of Akt3 prevents apoptotic cell death induced by
CC apoptotic stimulating kinase 1 (ASK1). The Akt3 polypeptide is useful
CC for inhibiting cell death, preferably in a cardiac myocyte, resulting
CC from hypoxia, apoptosis or necrosis in a patient suffering from
CC myocardial infarction or ischemia reperfusion injury. The polypeptide
CC is also useful for treating myocardial infarction or ischemia
CC reperfusion injury, where the reperfusion injury is myocardial ischemia
CC reperfusion injury or is associated with stroke, liver damage, renal
CC failure, organ transplantation or coronary artery by pass grafting.
XX
SQ Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;

Query Match 54.4%; Score 13.6; DB 21; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ccaacttggaatcacggtac 22
|||||||||| | |||||
Db 2 ccaacttggagaaatggtac 21

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